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### Integration of DNA Marker Information into Breeding Value Predictions

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# Integration of DNA Marker Information into Breeding Value Predictions

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## Summary

*Calves from 20 herds representing seven breeds were genotyped with a reduced DNA marker panel for weaning weight. The marker panel used was derived using MARC Cycle VII animals. The results suggest marker effects based on this small panel are not robust across breeds and that methodology exists to integrate genomic information into the prediction of breeding values in a single breed context.*

## Introduction

Currently, several commercial DNA tests (marker panels) are available for complex traits. In the fall of 2009, the American Angus Association integrated the results of an Angus-specific marker panel from a single commercial company into their national cattle evaluation for carcass traits. Despite this advancement, there still exists tremendous confusion by producers as to the efficacy of DNA diagnostics within and across breeds. The Weight Trait Project (WTP) was designed to address issues associated with creating and implementing DNA-based selection in conjunction with expected progeny differences (EPDs). The WTP is a unified effort among researchers, breed associations, seedstock producers, and a DNA testing company to improve the process of developing and validating DNA tests and to investigate the infrastructure necessary for the flow of information

needed to deliver Marker-Assisted EPDs to producers. Consequently, the objectives of the current study were to illustrate methodology for incorporating DNA marker information into breeding value predictions for the trait of weaning weight, and develop mechanisms for disseminating this information to producers.

## Procedure

Single nucleotide polymorphisms (SNPs), the smallest change in DNA sequence, for weaning weight were identified through an association study of markers on the Illumina 50K assay with weight traits collected at the U.S. Meat Animal Research Center (USMARC). The Illumina assay provides the opportunity to detect DNA variations at more than 50,000 locations across the cattle genome.

Weaning weight records (N = 3,328) of calves from the following populations were used in the selection at USMARC of SNPs associated with adjusted weaning weight. The total pedigree included 5,222 animals. Of the 3,328 calves in the training population, the average breed contributions were 26% Angus, 19% Hereford, and 6.5% each of Red Angus, Simmental, Charolais, Limousin, and Gelbvieh. Thus, the effective number of animals contributing to training by breed were 871 Angus, 632 Hereford, and 215 each of Red Angus, Simmental, Charolais, Limousin, and Gelbvieh.

Breed associations representing the seven breeds (Table 1) in the USMARC Cycle VII population identified seedstock producers in the region surrounding USMARC to provide DNA samples (hair follicles from the tail switch) from calves born in the 2009 calf crop and their dams. A reduced panel of 192 SNPs was constructed based on the most significant SNPs from the USMARC

association analysis with the addition of 192 SNPs from IGENITY<sup>®</sup> (96 trained on yearling weight in an Angus population and the other 96 from the IGENITY parentage panel). In total, the reduced panel consisted of 384 SNPs. IGENITY served as the genetic service provider partner in this project and genotyped animals with the reduced panel. After editing SNPs based on deviation from Hardy-Weinberg Equilibrium (a statistical criterion based on expected genotype frequencies), and call rates, a total of 159 of the diagnostic SNPs (not parentage) were used in the analysis. The population included over 19,000 animals from 20 seedstock enterprises and four university herds. Bull calves (n = 3,500) were genotyped with the reduced panel, and molecular breeding values (MBVs) were calculated based on prediction equations derived at USMARC for weaning weight (WW) and post-weaning gain (PWG). Data, including a four-generation pedigree, adjusted weaning weight phenotypes, and pedigree index EPDs were obtained from the respective breed associations for each herd in the project. MBVs were fit as a correlated trait in both two- and three-trait animal models. Contemporary group effects included herd and sex of calf. Weaning weight was fit with both a direct and maternal component while MBVs were assumed to have only a direct genetic component.

## Results

Heritabilities for weaning weight (direct and maternal) and MBVs (WW and PWG) by breed are summarized in Table 1. In general, the heritability estimates for WW direct were within expected ranges except for Simmental, which is likely due to the data structure of the Simmental herds in this study. Heritability estimates for

(Continued on next page)

both WW and PWG MBVs were lower than the expected value of 1.0, suggesting considerable error associated with prediction of MBVs, either due to genotyping error or low call rates. Genetic correlations between MBVs and weaning weight (direct and maternal) are presented in Table 2. In general, the genetic correlations are low to moderate with relatively large standard errors. The number of markers used in the current panel and the fact that almost half of the selected markers did not produce usable results might explain the poor performance and thus low genetic correlations. Given these correlations, the proportion of genetic variation for weaning weight explained by the panel ( $r_g^2$ ) ranged from 0 to 7.8%. One possible reason for the large range in genetic correlations among breeds is that the associations between markers and growth traits are more breed-specific than had been hoped.

### Implications

Results from the current study suggest that the reduced panel is not sufficient to meaningfully impact the accuracy of breeding value predictions. Furthermore, the unexpectedly low heritability estimates associated with the MBVs suggest that considerable room for improvement exists in

**Table 1. Heritabilities (SE) by breed for weaning weight (direct and maternal) and molecular breeding values (MBV) for weaning weight (WW) direct and post-weaning gain (PWG).**

Breed	Weaning Weight Direct	Weaning Weight Maternal	WW MBV	PWG MBV
Angus	0.23 (0.02)	0.12 (0.01)	0.87(0.16)	0.88 (0.16)
Red Angus	0.24 (0.03)	0.15 (0.02)	0.67 (0.16)	0.57 (0.14)
Charolais	0.12 (0.13)	0.08 (0.02)	0.33 (0.16)	0.32 (0.17)
Gelbvieh	0.22 (0.02)	0.08 (0.01)	0.64 (0.18)	0.38 (0.18)
Hereford	0.14 (0.04)	0.14 (0.04)	0.83 (0.15)	0.74 (0.19)
Limousin	0.27 (0.02)	0.10 (0.01)	0.60 (0.19)	0.72 (0.21)
Simmental	0.75 (0.03)	0.32 (0.02)	0.61 (0.16)	0.36 (0.15)

**Table 2. Genetic correlations (SE) by breed between weaning weight (direct and maternal) and molecular breeding values (MBV) for weaning weight (WW) and-post weaning gain (PWG).**

Breed	Weaning Weight Direct		Weaning Weight Maternal	
	WW MBV	PWG MBV	WW MBV	PWG MBV
Angus	0.00 (0.10)	0.14 (0.10)	0.00 (0.17)	-0.04 (0.17)
Red Angus	0.10 (0.10)	0.35 (0.09)	0.02 (0.16)	-0.18 (0.15)
Charolais	0.28 (0.15)	-0.06 (0.17)	0.14 (0.20)	0.05 (0.22)
Gelbvieh	0.25 (0.13)	0.25 (0.12)	-0.22 (0.22)	-0.03 (0.22)
Hereford	0.20 (0.20)	0.29 (0.20)	0.06 (0.28)	-0.06 (0.29)
Limousin	0.24 (0.12)	0.18 (0.12)	-0.53 (0.22)	-0.08 (0.23)
Simmental	-0.05 (0.08)	-0.06 (0.08)	0.22 (0.13)	0.19 (0.12)

the genotyping platform. Although the standard errors associated with the genetic correlations are large, the point estimates do vary across breeds. The current project developed a unique and vast resource for the future development of methodology related to the incorporation of marker data into national cattle evaluations utilizing resources from researchers, extension personnel, producers, breed

associations, and a commercial DNA testing company.

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